THE UNIVERSITY
of NORTH CAROLINA
at CHAPEL HILL

SPHARM-PDM

User Tutorial

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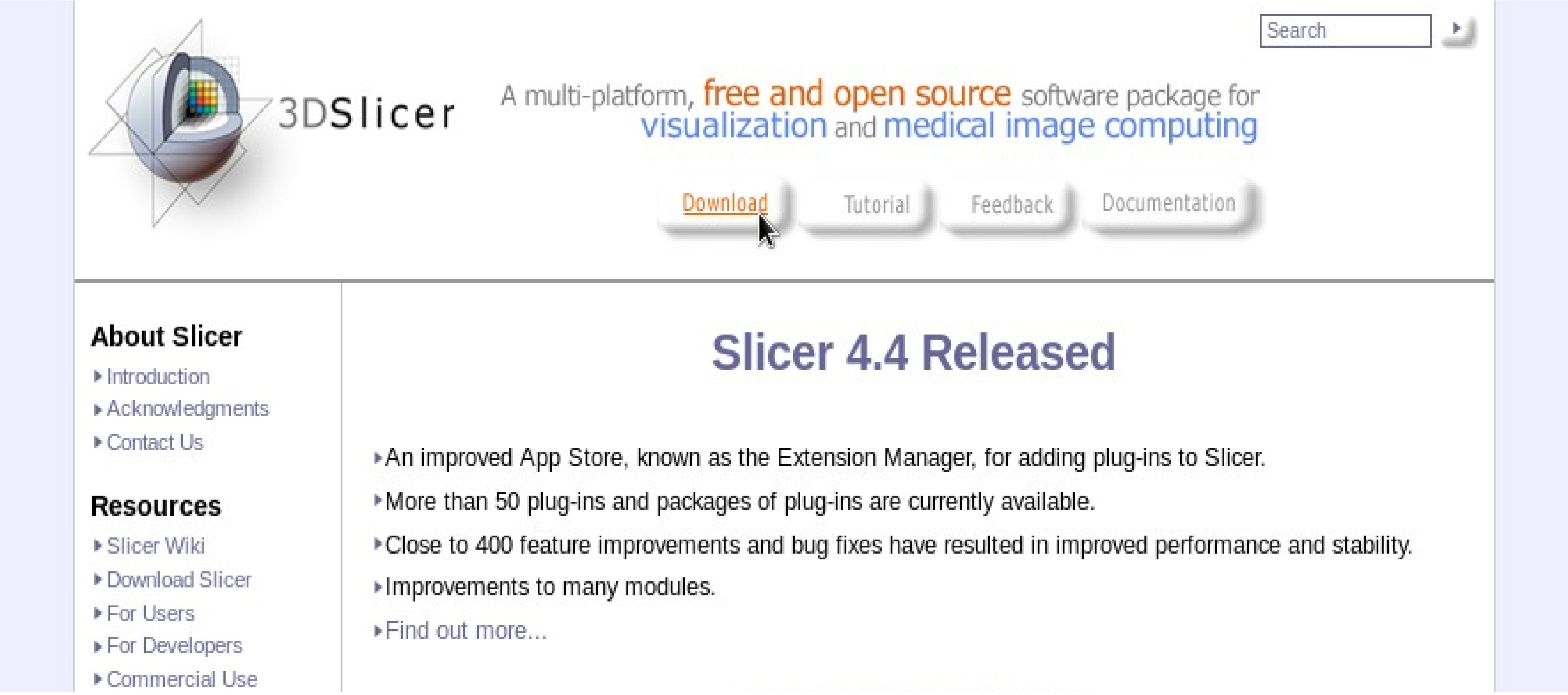
July 2015

3D Slicer Installation

- Go to www.slicer.org to download Slicer for your respective operating system.

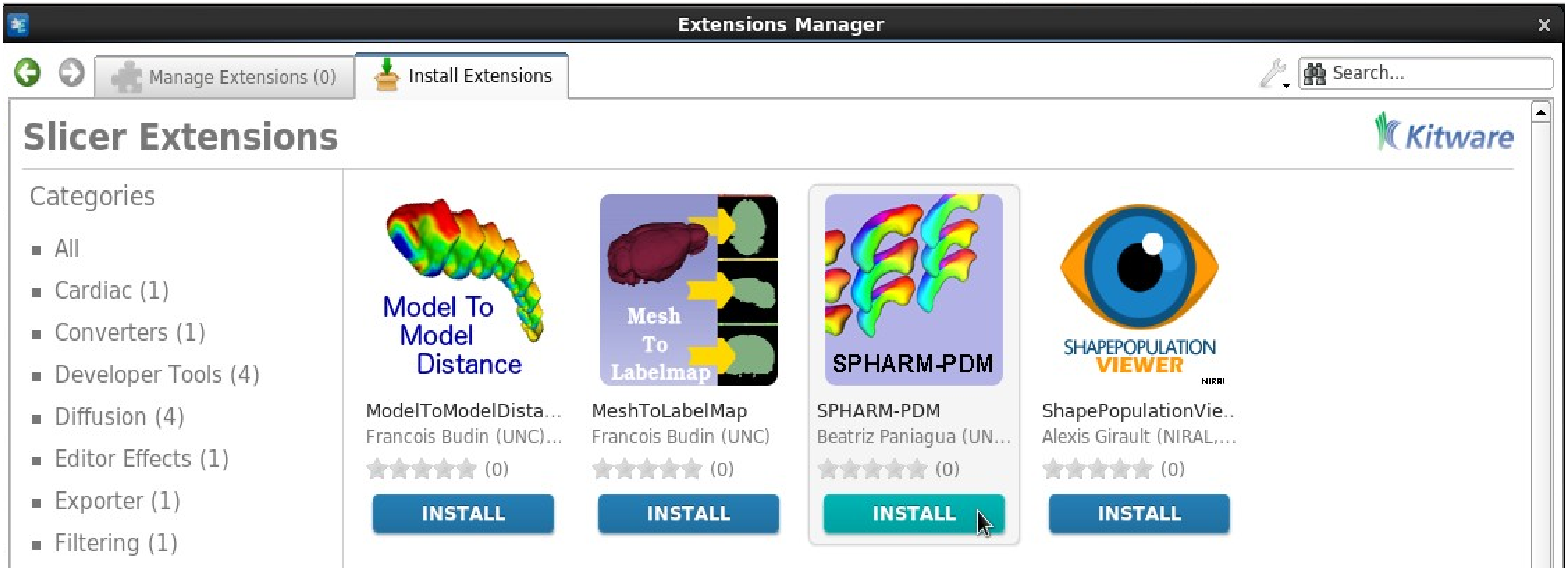


Slicer 4.4 Released

- An improved App Store, known as the Extension Manager, for adding plug-ins to Slicer.
- More than 50 plug-ins and packages of plug-ins are currently available.
- Close to 400 feature improvements and bug fixes have resulted in improved performance and stability.
- Improvements to many modules.
- Find out more...

SPHARM-PDM Installation

- In 3D Slicer, go to *View -> Extension Manager*
- In the *Install Extensions* tab, select *Shape Analysis* under *Categories*.
- Under SPHARM-PDM, select the *Install* button and restart Slicer when prompted.

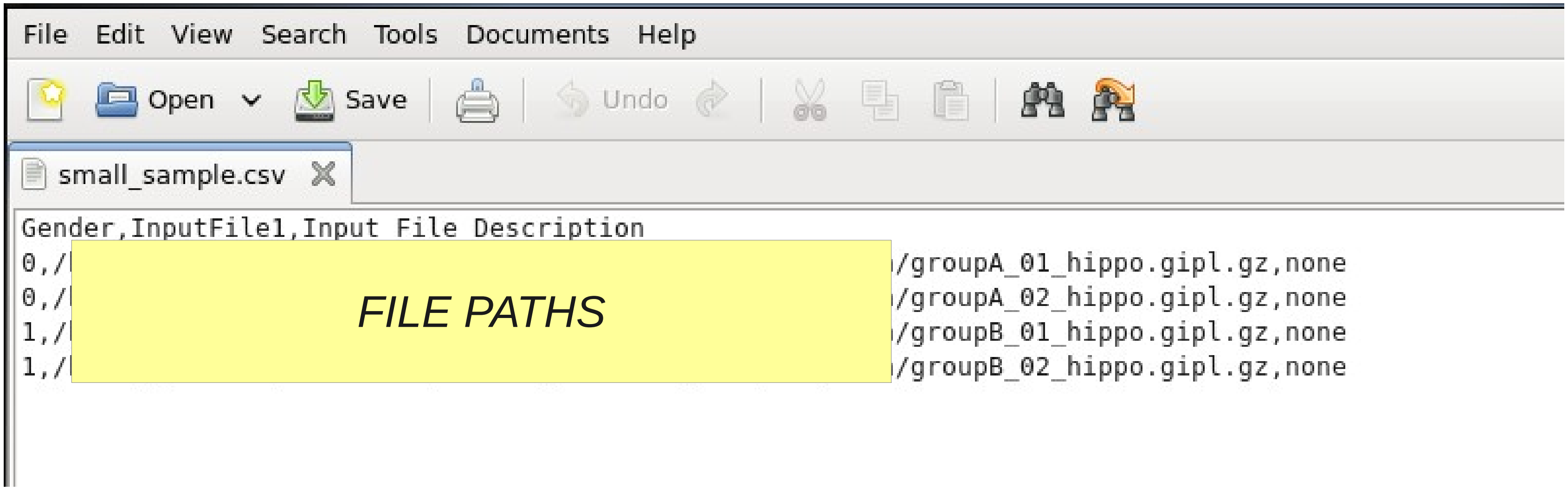


ShapePopulationViewer

- For quality control, we analyze our SPHARM-PDM outputs with the *ShapePopulationViewer* extension.
- To install *ShapePopulationViewer*, go back to the *Install Extensions* tab and select *Shape Analysis* under *Categories*.
- Select the appropriate *Install* button and restart Slicer when prompted.

Input File (from provided dataset)

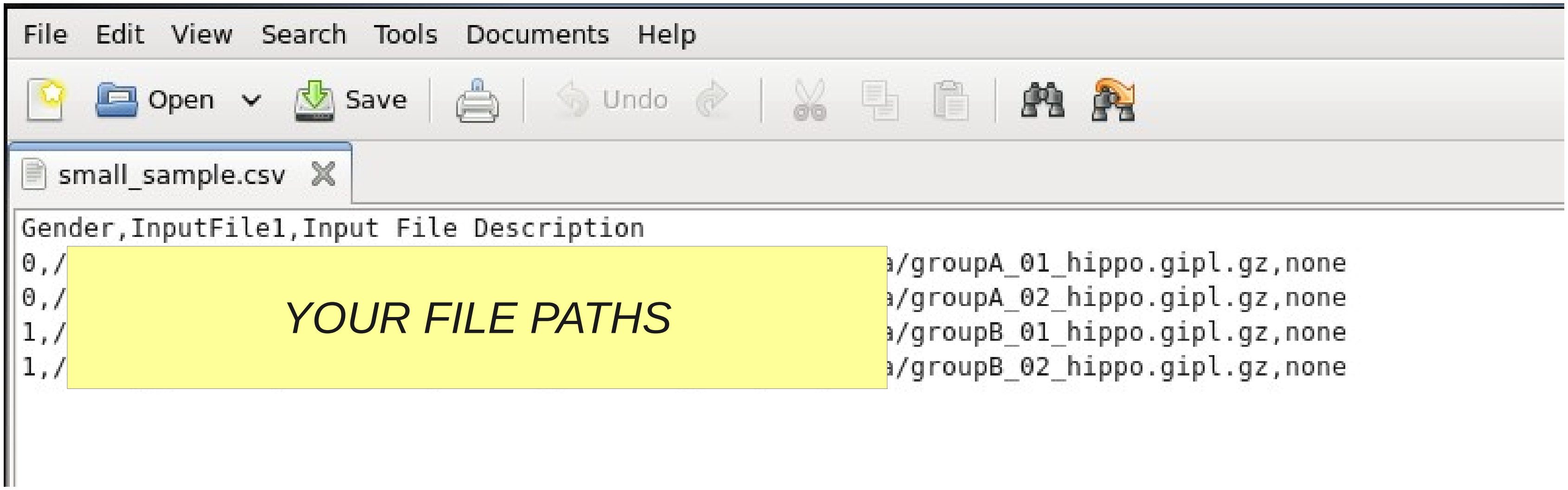
- Download and unzip the data for this tutorial from https://www.nitrc.org/docman/view.php/308/1981/SPHARM_Tutorial_Data_July2015.zip
- We will start out with a small CSV file: small_sample.csv
- A small file will let the program run quickly and will allow you to easily see the basic features of SPHARM-PDM.
- In the *SPHARM_Tutorial_Data_July2015* folder, open small_sample.csv in gedit or a similar word processing program.
- The first row of the CSV file should be the header labels of the columns. The rows that follow represent the data.



```
Gender,InputFile1,Input File Description
0,/[redacted]/groupA_01_hippo.gipl.gz,none
0,/[redacted]/groupA_02_hippo.gipl.gz,none
1,/[redacted]/groupB_01_hippo.gipl.gz,none
1,/[redacted]/groupB_02_hippo.gipl.gz,none
```

Input File (from provided dataset)

- Replace the path of each data file location in this file with its current path on your computer, making sure to maintain the format of the original data.

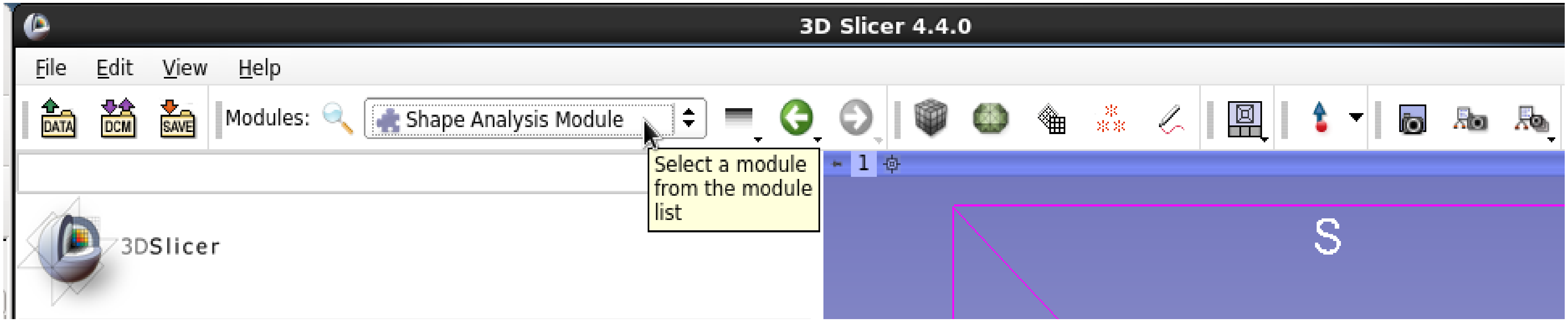


```
Gender,InputFile1,Input File Description
0,/                                              /groupA_01_hippo.gipl.gz,none
0,/                                              /groupA_02_hippo.gipl.gz,none
1,/                                              /groupB_01_hippo.gipl.gz,none
1,/                                              /groupB_02_hippo.gipl.gz,none
```

YOUR FILE PATHS

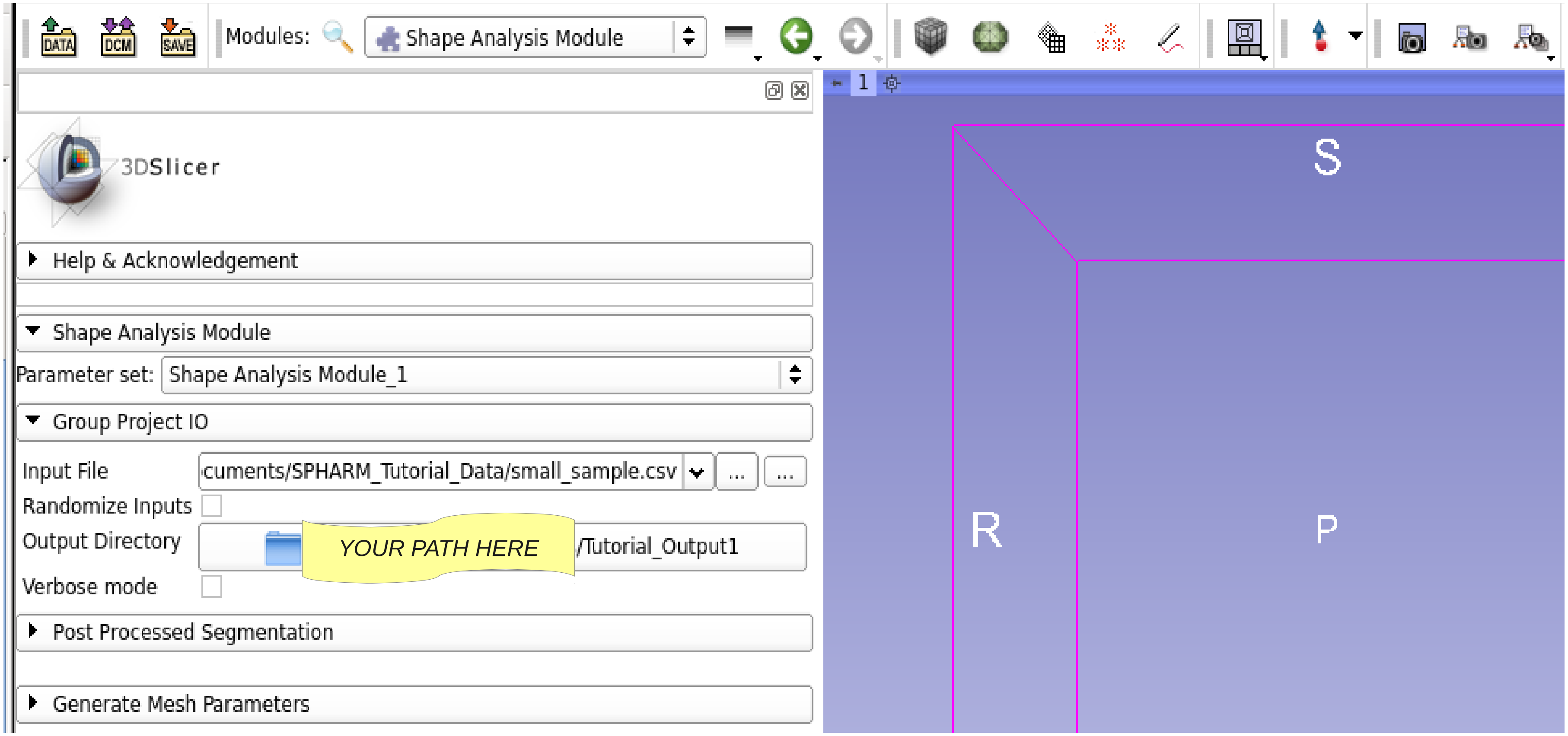
Initializing the Module

- In Slicer, select *Shape Analysis Module* from the *Modules* drop-down menu.



Setting up Input and Output

- In the *Shape Analysis Module* under the *Group Project IO* tab, for *Input File* select the CSV file we modified earlier.
- For *Output Directory* create a folder named *Tutorial_Output1* where the *small_sample.csv* output data will be sent.



Parameter set: Shape Analysis Module_1

Input File: cuments/SPHARM_Tutorial_Data/small_sample.csv

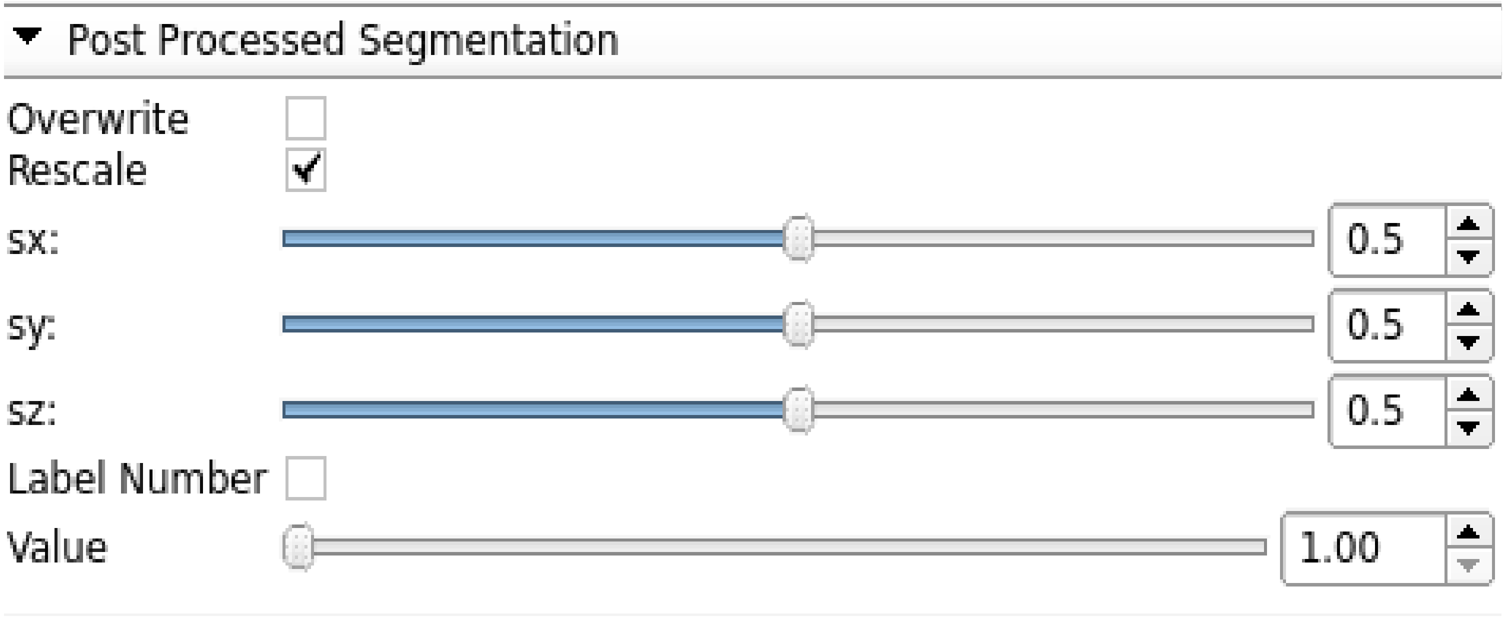
Randomize Inputs ☐

Output Directory: YOUR PATH HERE /Tutorial_Output1

Verbose mode ☐

Features and Parameters

- Let's look under the *Post Processed Segmentation* tab.
- The X, Y and Z spacing parameters (*sx/sy/sz*) determine the resolution in which the data will be processed for each axis (in millimeters).

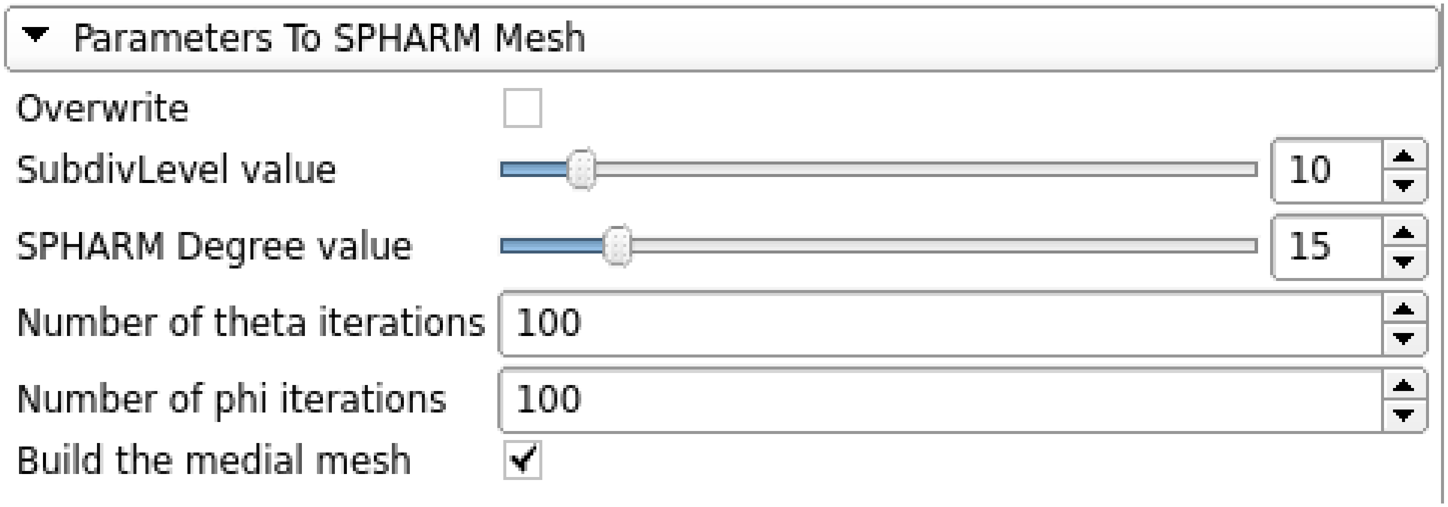


Post Processed Segmentation

Overwrite ☐
Rescale ☑
sx: 0.5
sy: 0.5
sz: 0.5
Label Number ☐
Value 1.00

Features and Parameters

- Let's look under the *Parameters To SPHARM Mesh* tab.
- Icosahedron subdivision allows for linear, uniform sampling of the object by referring to its spherical parameterization. The *SubdivLevel value* sets the level of the subdivision factor that will be used.



▾ Parameters To SPHARM Mesh

Overwrite ☐

SubdivLevel value 10

SPHARM Degree value 15

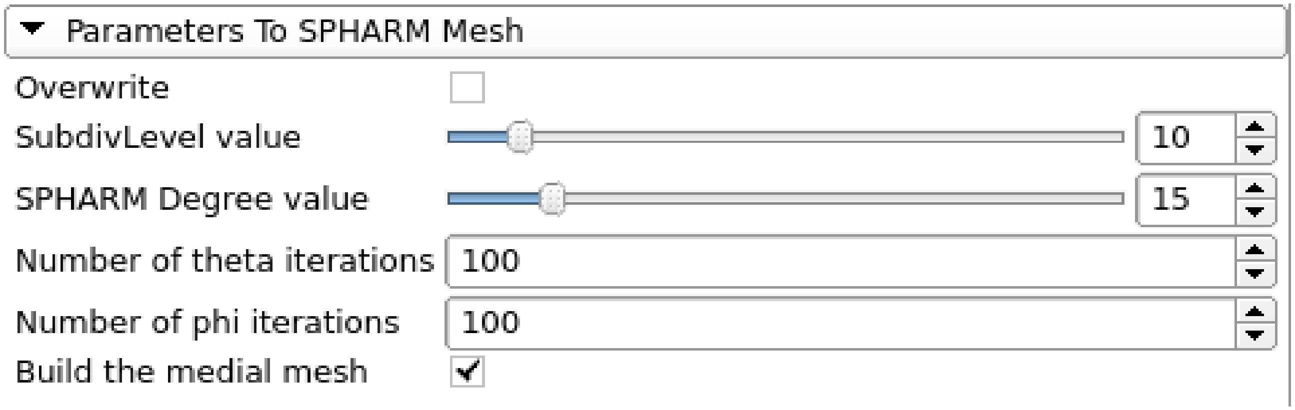
Number of theta iterations 100

Number of phi iterations 100

Build the medial mesh ☑

Features and Parameters

- The *SPHARM Degree value* represents the degree of the spherical harmonic series used on the data. Changing this value results in different levels of detail of the object. We can leave it at its default value of 15 which will give us a sufficiently high representation level for the structures provided as example data.
- If the *Build the medial mesh* option is checked, SPHARM-PDM will compute the mean latitude axis associated with the data. The *Number of theta/phi iterations* corresponds to the number of samples used in the medial mesh computation[1].



Parameters To SPHARM Mesh

Overwrite ☐
SubdivLevel value 10
SPHARM Degree value 15
Number of theta iterations 100
Number of phi iterations 100
Build the medial mesh ☑

---

[1] *Paniagua B1, Lyall A, Berger JB, Vachet C, Hamer RM, Woolson S, Lin W, Gilmore J, Styner M. (2013). Lateral ventricle morphology analysis via mean latitude axis. Proc SPIE Int Soc Opt Eng. 2013 Mar 29;8672. pii: 2006846. <http://www.ncbi.nlm.nih.gov/pubmed/23606800>*

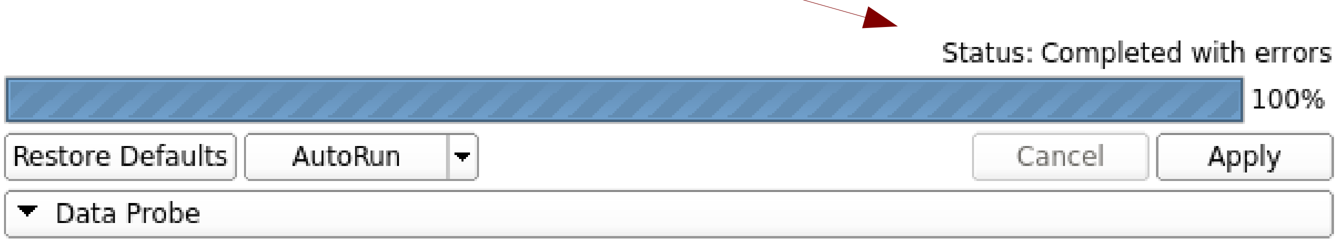
Running SPHARM-PDM

- At the bottom of the Shape Analysis Module, click *Apply* to run SPHARM-PDM on the inputs we provided.

- The Module will signify when it has completed.

Running SPHARM-PDM

- If SPHARM-PDM encounters any errors, the Module will alert you once it has finished running.

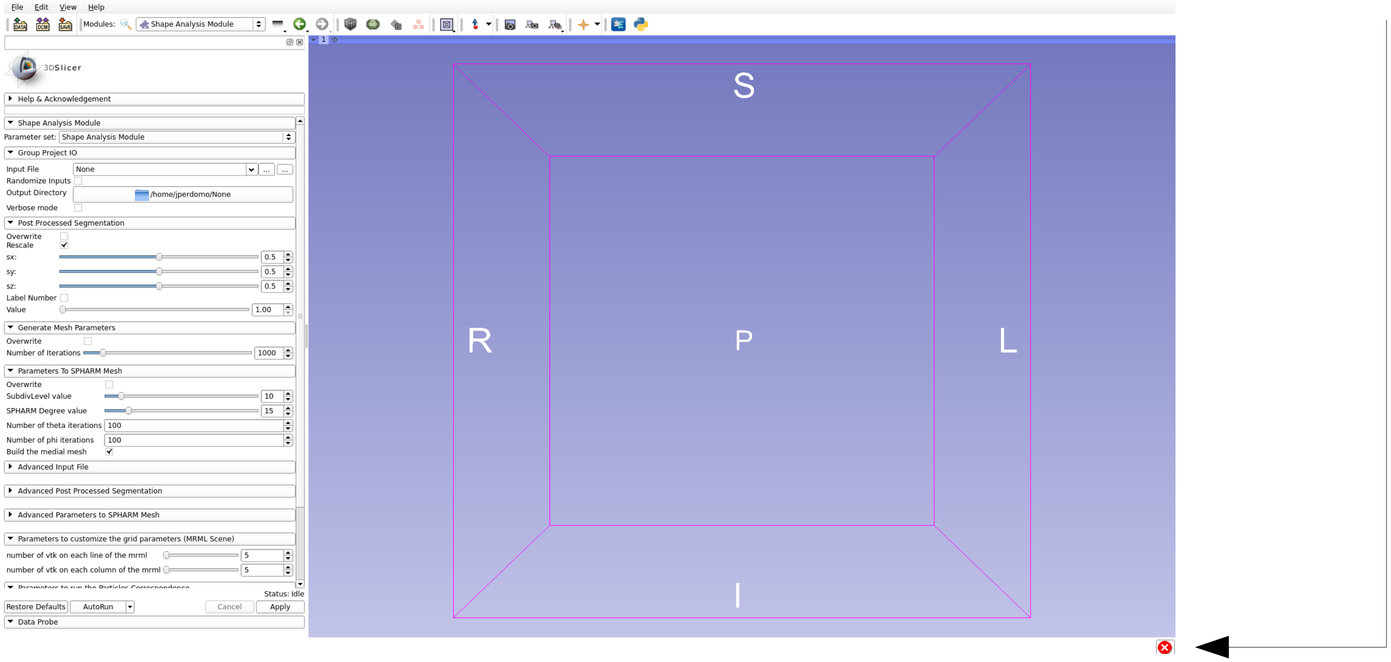


Status: Completed with errors

- For debugging, we can use 3D Slicer's *Error Log* feature.

Debugging

- To open 3D Slicer's *Error Log*, click on the red icon at the bottom right.



Help & Acknowledgement

Shape Analysis Module

Parameter set: Shape Analysis Module

Group Project IO

Input File None

Randomize Inputs ☐

Output Directory /home/jperdomo/None

Verbose mode ☐

Post Processed Segmentation

Overwrite ☐

Rescale ☑

sx: 0.5

sy: 0.5

sz: 0.5

Label Number ☐

Value 1.00

Generate Mesh Parameters

Overwrite ☐

Number of Iterations 1000

Parameters To SPHARM Mesh

Overwrite ☐

SubdivLevel value 10

SPHARM Degree value 15

Number of theta iterations 100

Number of phi iterations 100

Build the medial mesh ☑

Advanced Input File

Advanced Post Processed Segmentation

Advanced Parameters to SPHARM Mesh

Parameters to customize the grid parameters (MRML Scene)

number of vtk on each line of the mrml 5

number of vtk on each column of the mrml 5

Status: Idle

Restore Defaults | AutoRun | Cancel | Apply

Data Probe

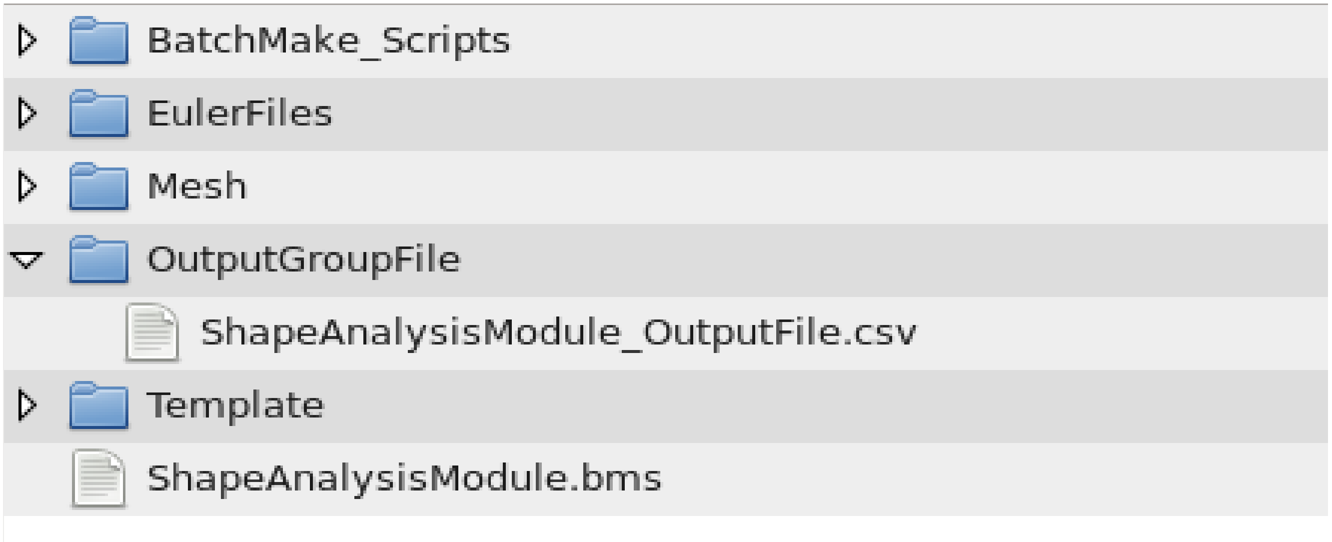
- This brings up 3D Slicer's *Log messages* dialog box with information about warnings, messages, and errors.

Output Files

- Navigate to the output folder *Tutorial_Output1* in your computer. This is where the output of SPHARM-PDM has been stored.
- The *BatchMake_Scripts* folder is outdated and will be removed in the next version.
- The *EulerFiles* folder contains the Euler characteristic information of the data. The Euler characteristic is a number that is used to describe the topology of an object. Spherical topology has a Euler number of 2.
- The *Mesh* folder contains the mesh and surface data that resulted from the SPHARM-PDM analysis. We will look into its sub-folders later.

Output Files

- The *OutputGroupFile* folder contains a CSV file of all the output data.
  - This CSV can load directly into *ShapePopulationViewer* for quality control.
- The *Template* folder contains the information for the data file that was used as a template. By default this is the first data file that was processed.



BatchMake_Scripts
EulerFiles
Mesh
OutputGroupFile
  ShapeAnalysisModule_OutputFile.csv
Template
ShapeAnalysisModule.bms

Output Files

- The *Mesh* folder contains all of the surface and mesh output data which corresponds to the processes outlined by the diagram below.

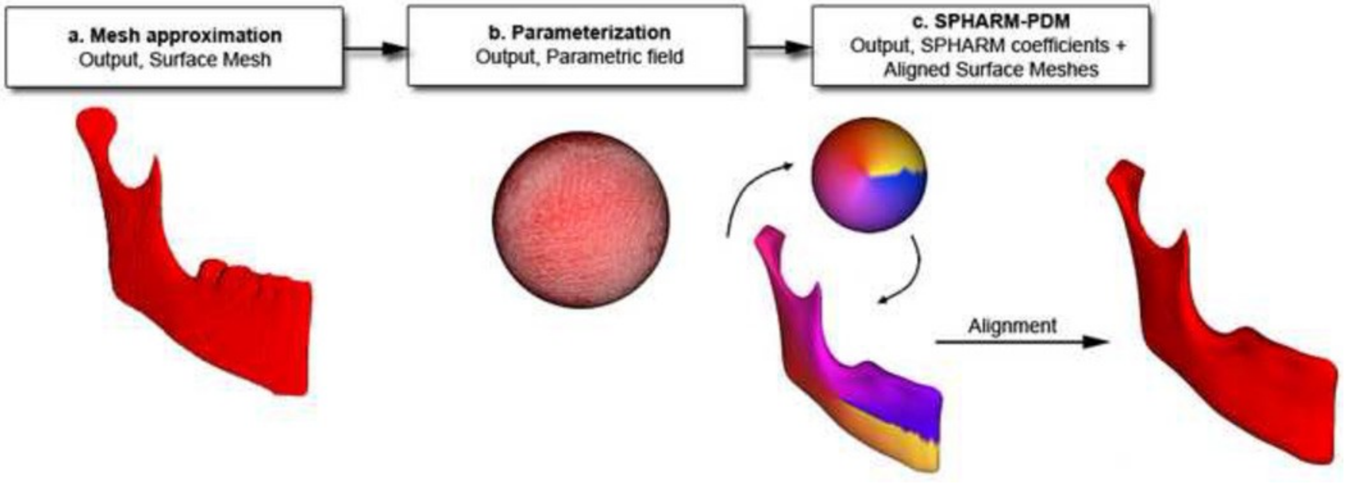
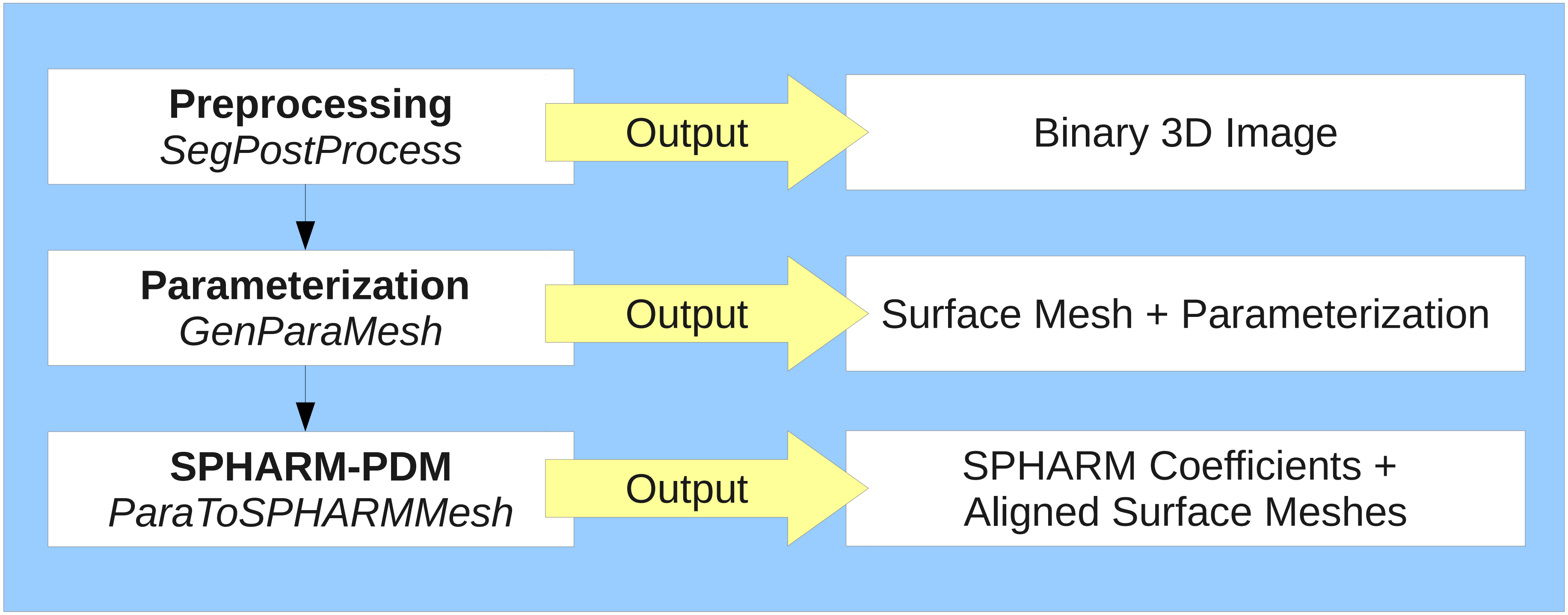


Image source:

Cevidanes, L. H. S., Alhadidi, A., Paniagua, B., Styner, M., Ludlow, J., Mol, A., … Rossouw, P. E. (2011). 3D Quantification of Mandibular Asymmetry through Cone Beam Computed Tomography. Oral Surgery, Oral Medicine, Oral Pathology, Oral Radiology, and Endodontics, 111(6), 757–770. doi:10.1016/j.tripleo.2011.02.002

Output Files

- The SPHARM-PDM processes are further outlined in the diagram below.



Preprocessing
SegPostProcess

Output

Binary 3D Image

Parameterization
GenParaMesh

Output

Surface Mesh + Parameterization

SPHARM-PDM
ParaToSPHARMMesh

Output

SPHARM Coefficients +
Aligned Surface Meshes

Output Files

- The *Mesh* folder has two sub-folders, *PostProcess* and *SPHARM*. The *PostProcess* sub-folder contains surfaces aligned with SPHARM.

PostProcess
groupA_01_hippo_pp.gipl.gz
groupA_02_hippo_pp.gipl.gz
groupB_01_hippo_pp.gipl.gz
groupB_02_hippo_pp.gipl.gz

Preprocessing
SegPostProcess

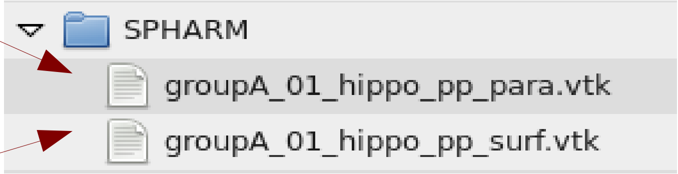
Output

Binary 3D Image

Output Files

- The first two output files in the *SPHARM* sub-folder are:

1) **para.vtk*, a spherical parameterization of the input data file. The surface data of the input file is mapped to a sphere.
2) **surf.vtk*, a surface approximation of the input file. The surface will appear blocky because of the absence of spherical harmonics (SPHARM).



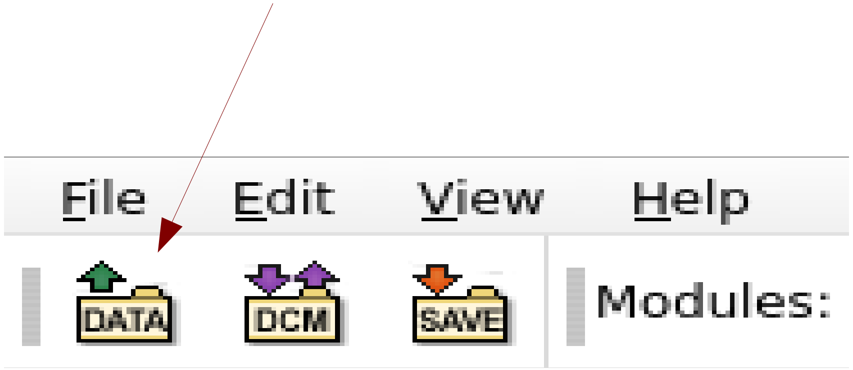
- SPHARM
  - groupA_01_hippo_pp_para.vtk
  - groupA_01_hippo_pp_surf.vtk

Parameterization
GenParaMesh

Output → Surface Mesh + Parameterization

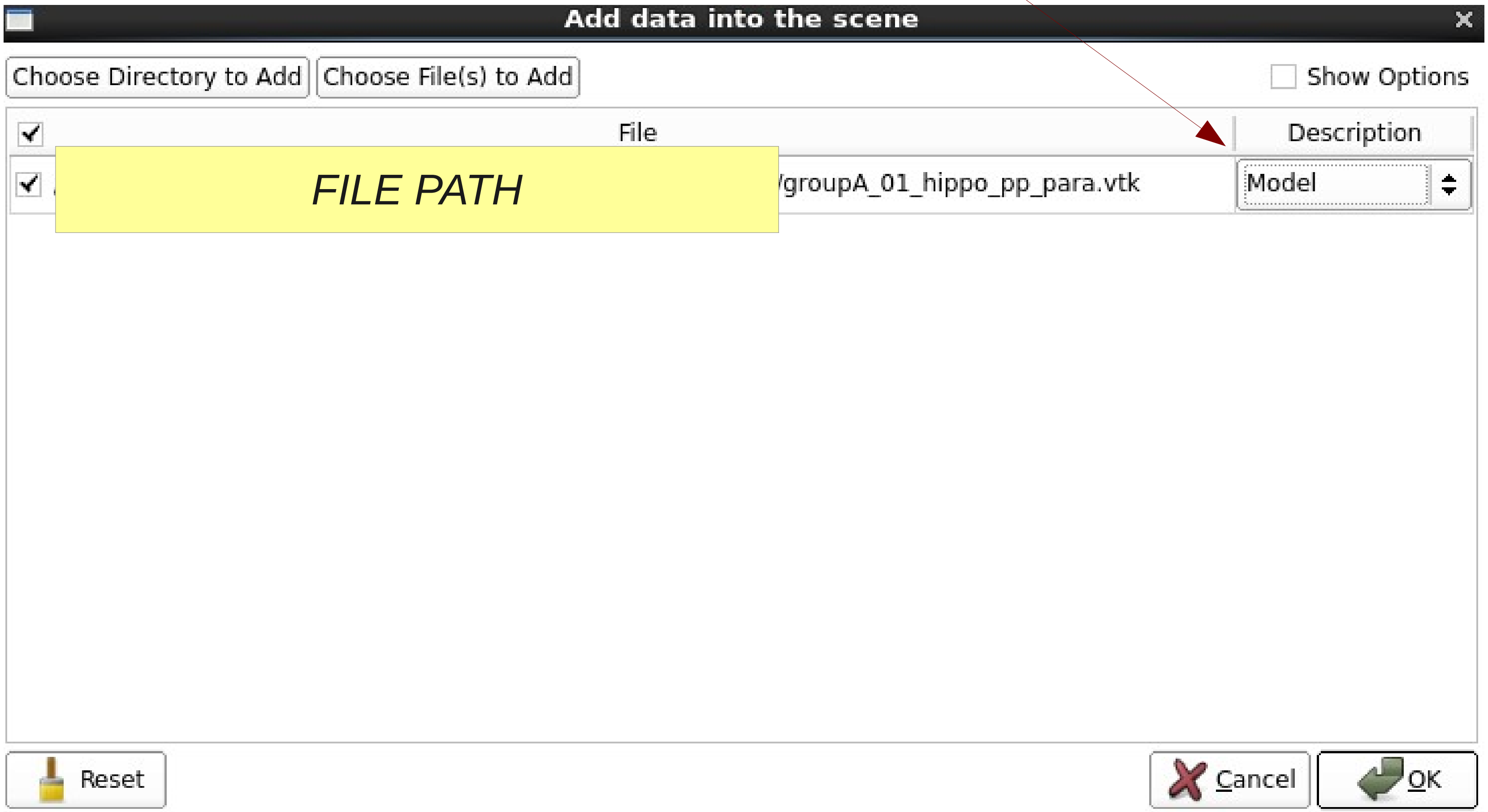
Viewing VTK files in Slicer

- VTK files can be viewed in Slicer by simply dragging and dropping the file into the program or by using the *Data* button in the toolbar to search for the file.



Viewing VTK files in Slicer

- Make sure the *Model* option is selected under the *Description* column when importing the VTK file.

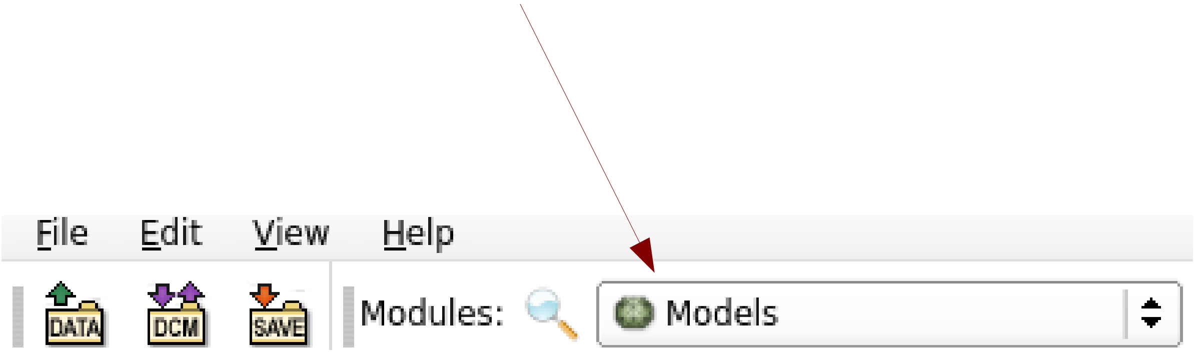


☑ FILE PATH /groupA_01_hippo_pp_para.vtk

Description: Model

Viewing VTK files in Slicer

- Once your VTK file has been imported, it will be visualized in the *Scene View* on the right side of the program. Switch to the *Models* Module to change the display settings of the VTK model.



Viewing VTK files in Slicer

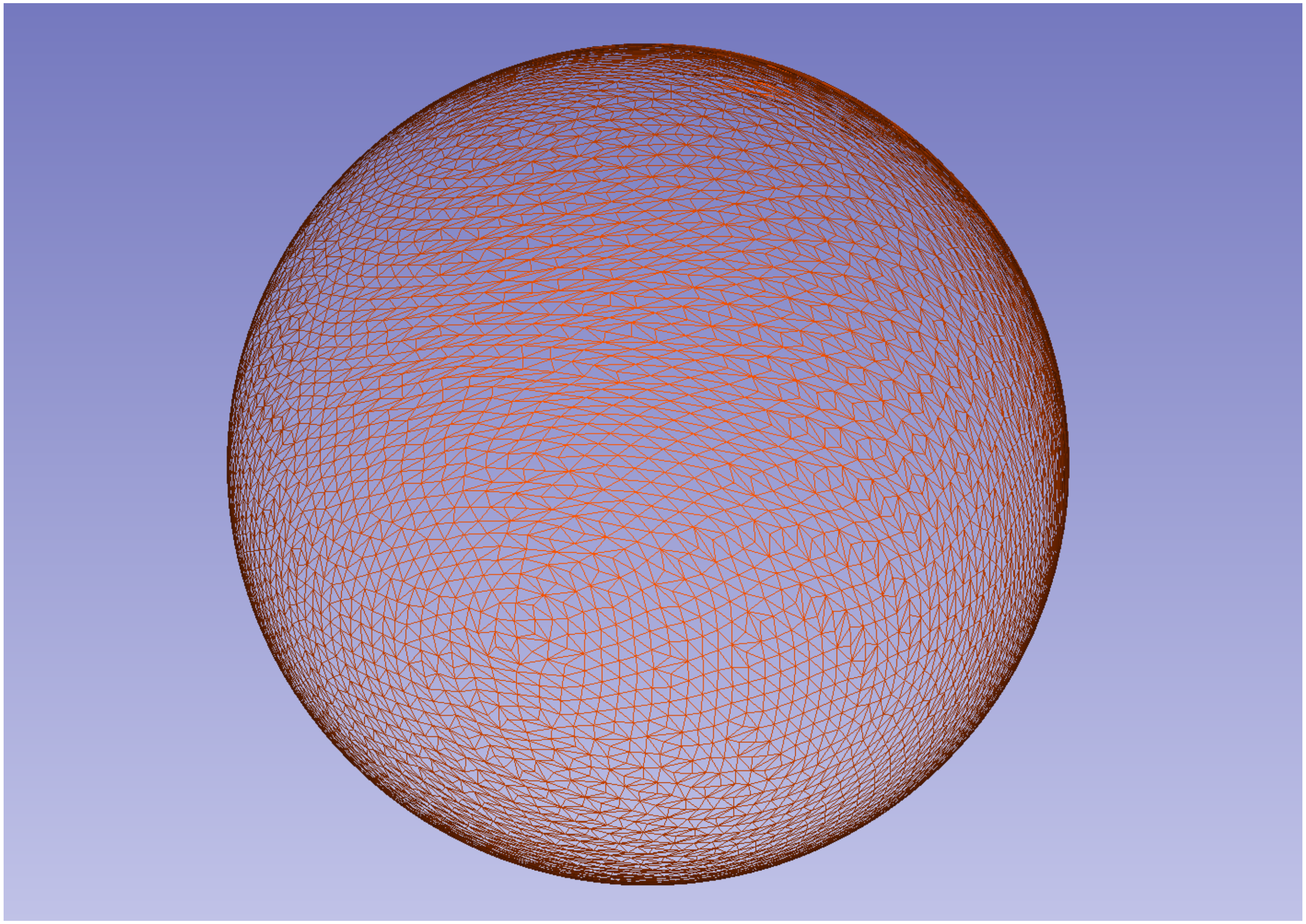
- To change the display properties of the VTK file, first select the file from the *Scene* window in the *Models* Module.
- Now you can apply different properties that will appear in the *Scene View*.
- For the **para.vtk* file in the next slide, I changed the *Representation* from *Surface* to *Wireframe* for more detail.
- I also changed the *Color* setting from the default gray color to a bright orange color.

groupA_01_hippo_pp_para 🟩 1.00

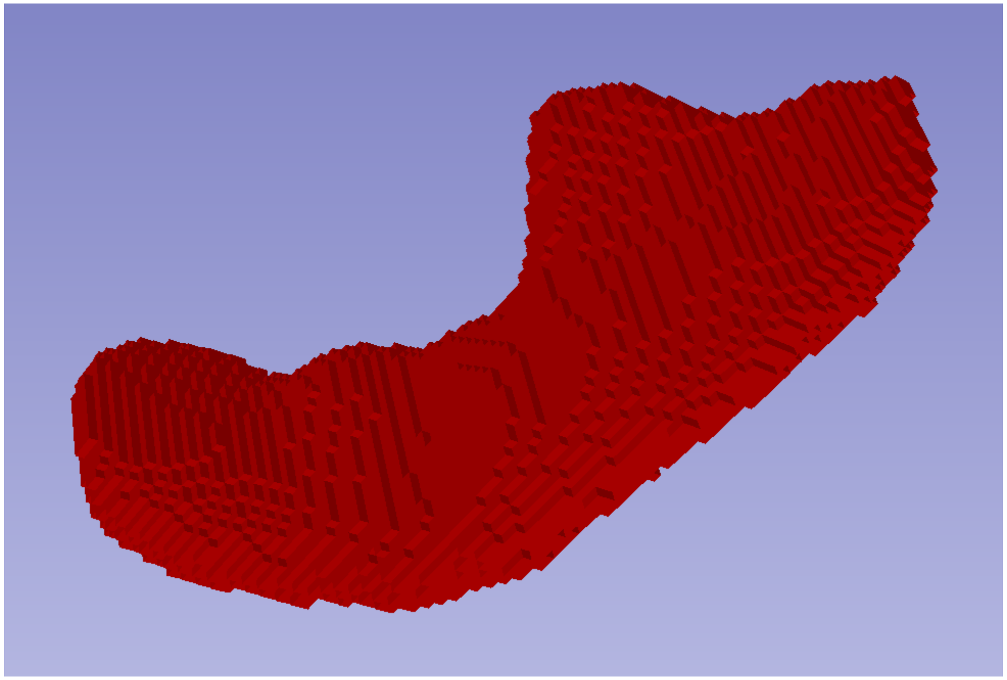
Representation: Wireframe
Point Size: 1.00
Line Width: 1.00
Culling: ☐ Frontface ☑ Backface

Color: 🟩 #00aa00
Opacity: 1.00
Edge Visibility: ☐
Edge Color: ■ #000000

para.vtk



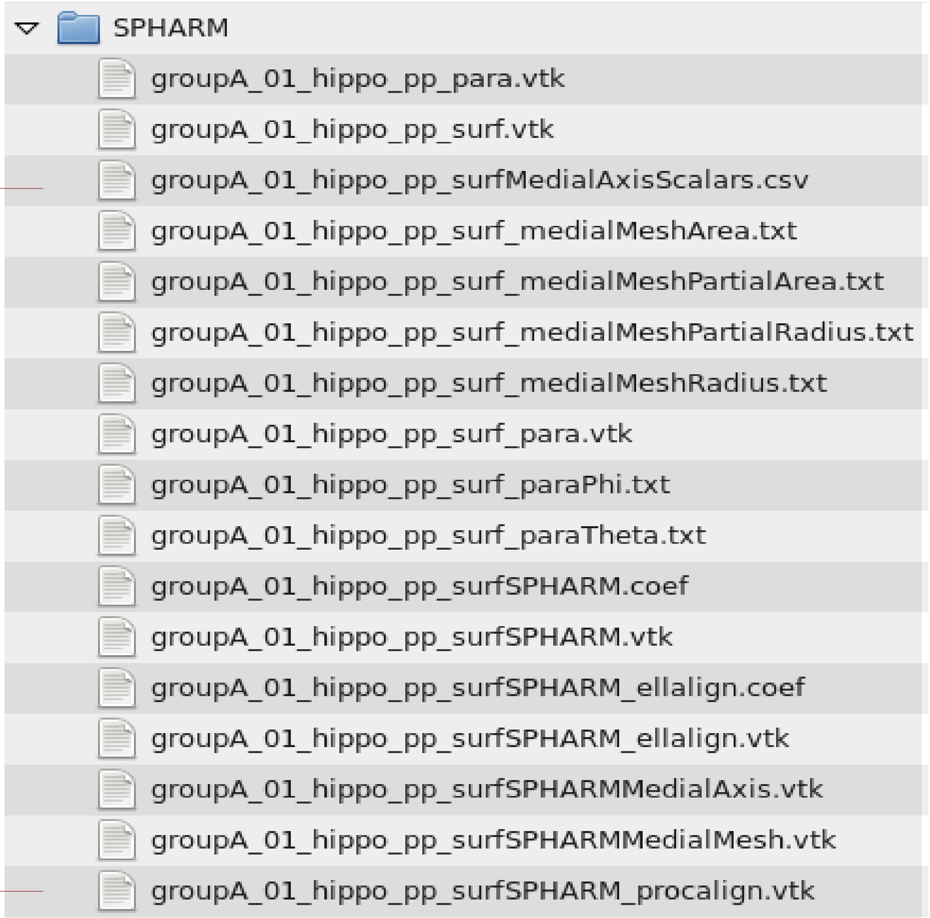
**surf.vtk*



- Note the blocky surface of the **surf.vtk* file. This is because the **surf.vtk* file represents the original voxel mesh. The cubes show the voxel delineation.

SPHARM-PDM Outputs

- Let's look at the files for *groupA_01*.
- After the parameterizations are calculated, SPHARM-PDM runs *ParaToSPHARMMesh*, which gives you the final SPHARM-PDM outputs.



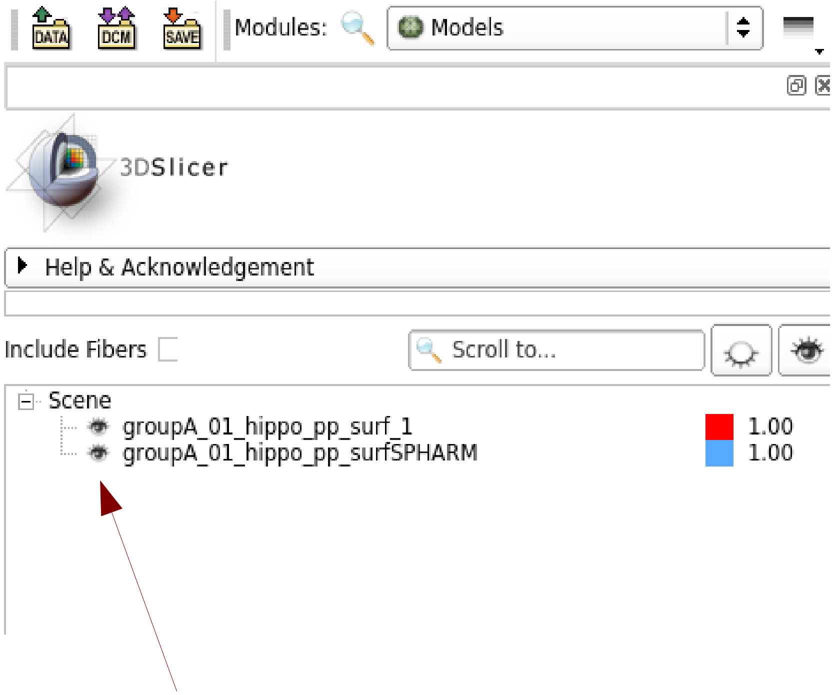
SPHARM
groupA_01_hippo_pp_para.vtk
groupA_01_hippo_pp_surf.vtk
groupA_01_hippo_pp_surfMedialAxisScalars.csv
groupA_01_hippo_pp_surf_medialMeshArea.txt
groupA_01_hippo_pp_surf_medialMeshPartialArea.txt
groupA_01_hippo_pp_surf_medialMeshPartialRadius.txt
groupA_01_hippo_pp_surf_medialMeshRadius.txt
groupA_01_hippo_pp_surf_para.vtk
groupA_01_hippo_pp_surf_paraPhi.txt
groupA_01_hippo_pp_surf_paraTheta.txt
groupA_01_hippo_pp_surfSPHARM.coef
groupA_01_hippo_pp_surfSPHARM.vtk
groupA_01_hippo_pp_surfSPHARM_ellalign.coef
groupA_01_hippo_pp_surfSPHARM_ellalign.vtk
groupA_01_hippo_pp_surfSPHARMMedialAxis.vtk
groupA_01_hippo_pp_surfSPHARMMedialMesh.vtk
groupA_01_hippo_pp_surfSPHARM_procalign.vtk

SPHARM-PDM
ParaToSPHARMMesh

Output

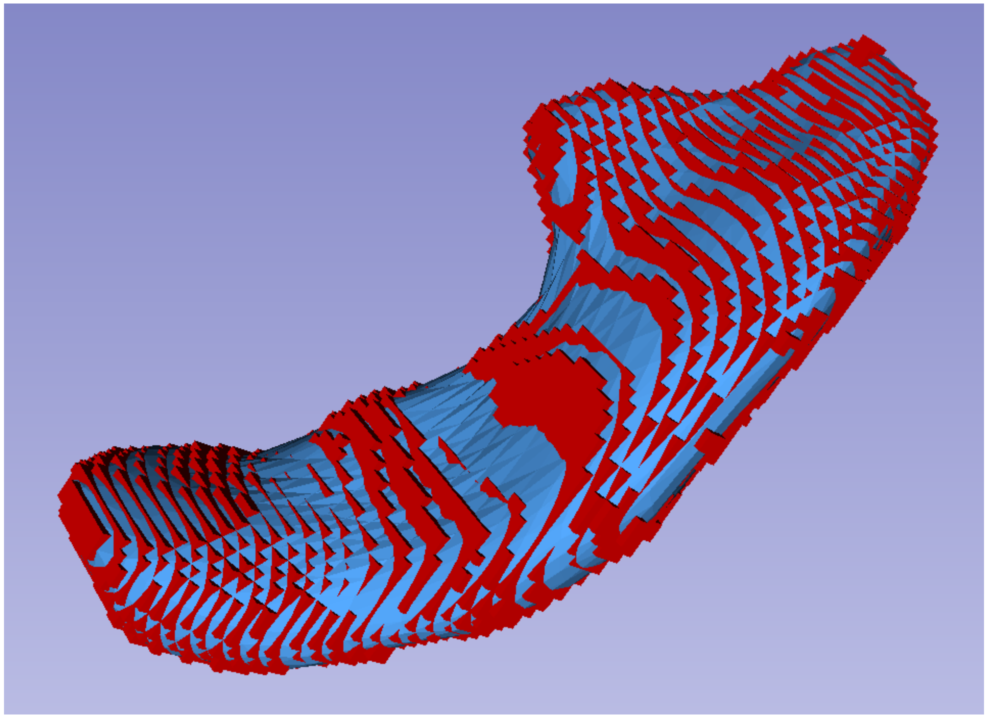
SPHARM Coefficients +
Aligned Surface Meshes

*surf.vtk & *surfSPHARM.vtk



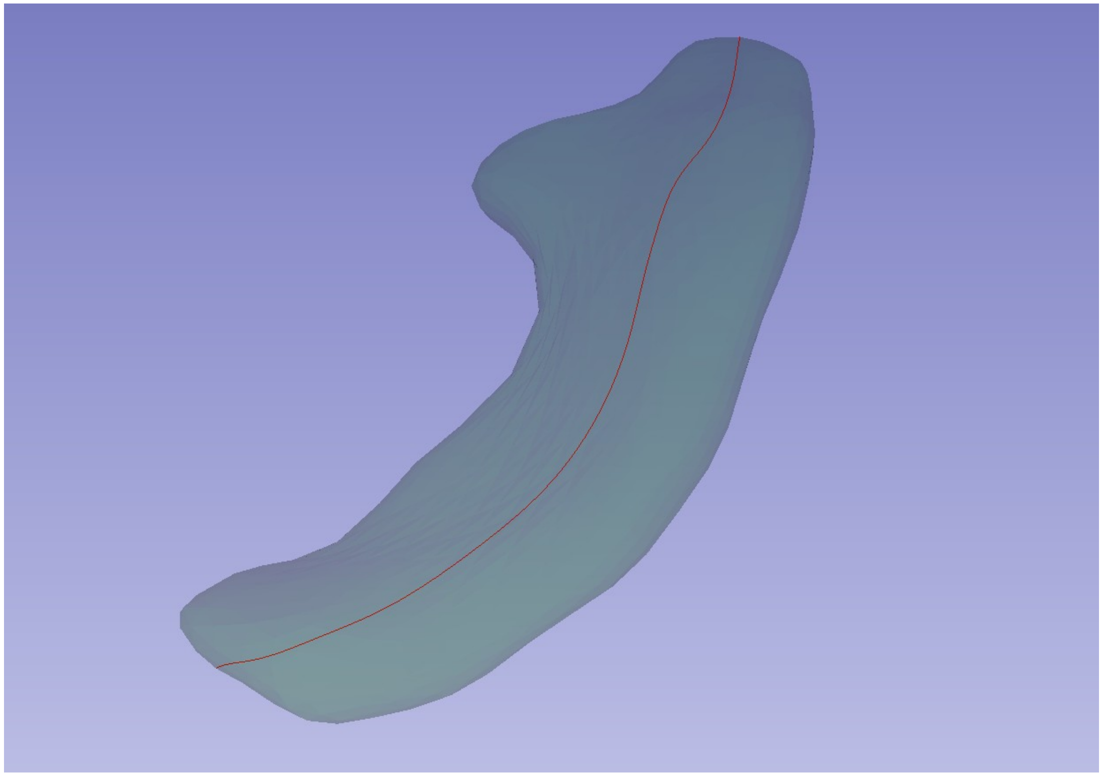
Modules: Models

Scene
- groupA_01_hippo_pp_surf_1 🟥 1.00
- groupA_01_hippo_pp_surfSPHARM 🟦 1.00



- This is a comparison of *surf.vtk* (red) and *surfSPHARM.vtk* (light blue). The visibility of a loaded VTK file in the *Scene View* can be toggled by clicking the eye icon next to its name in the *Models* module.

*surfSPHARM_procalign.vtk & *surfSPHARMMedialAxis.vtk



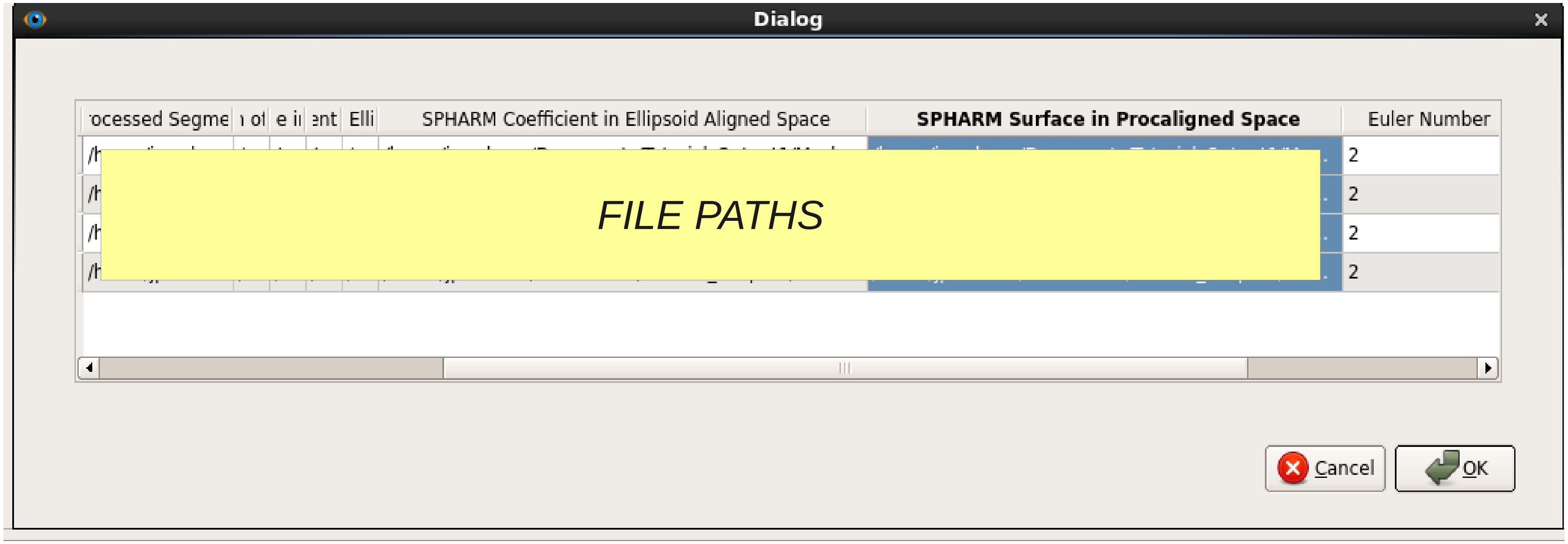
- This is a comparison of the calculated medial axis, *surfSPHARMMedialAxis.vtk* (red), and the Procrustes-aligned *surfSPHARM_procalign.vtk* file (green). Note that you can change the opacity of VTK files within the *Models* module for these comparisons.

Quality control using ShapePopulationViewer

- The *ShapePopulationViewe*r extension can be opened within Slicer.
- In the *Modules* drop-down menu, go to *Shape Analysis* -> *ShapePopulationViewer*.
- This opens the *ShapePopulationViewer* module in Slicer.
- Click *Apply* in the module to open a new *ShapePopulationViewer* window.

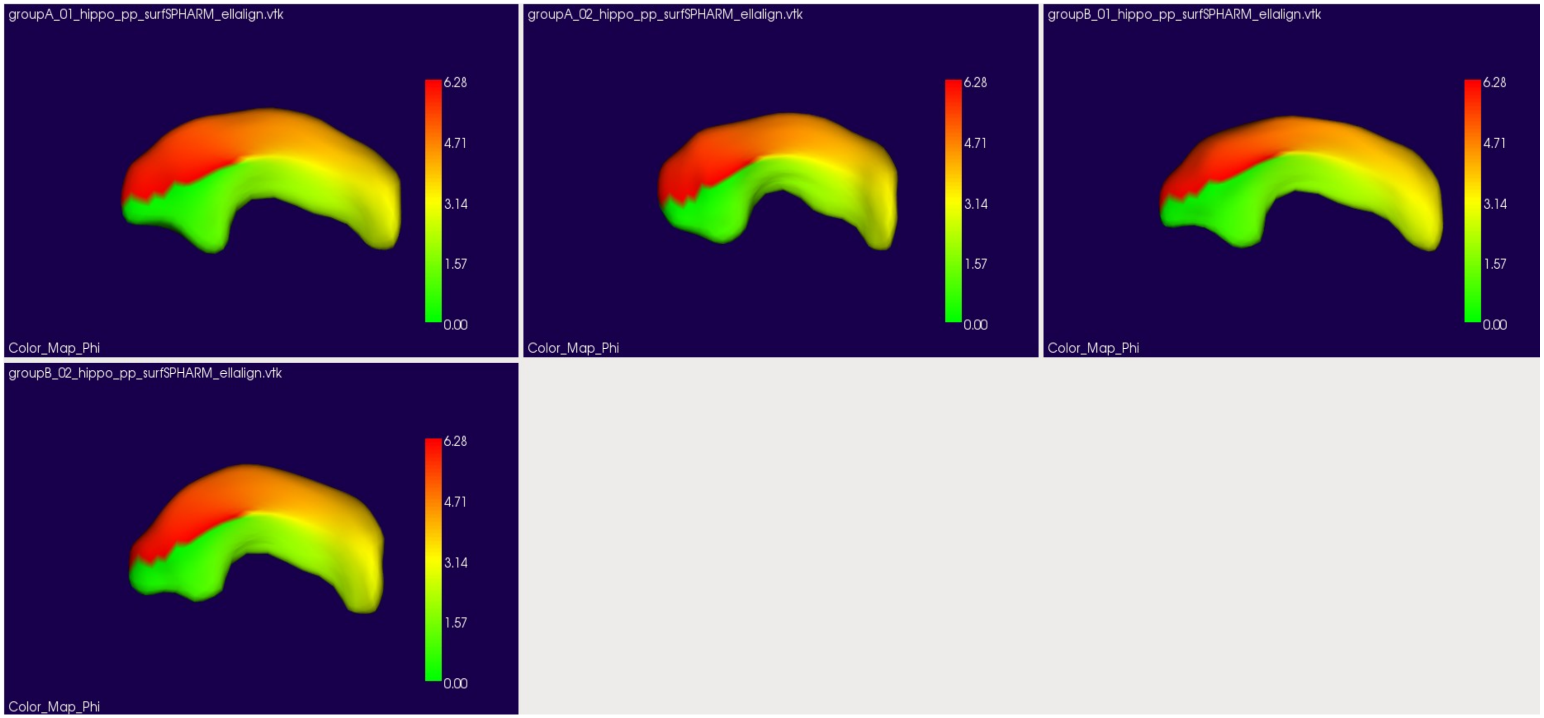
Quality control using ShapePopulationViewer

- In *ShapePopulationViewer*, go to *File -> Load CSV*.
- In the pop-up window, find your *Tutorial_Output1* folder and select the group CSV file within the *OutputGroupFile* folder.
- In the next window, select the column titled *SPHARM Surface in Procaligned Space* to select all the SPHARM-PDM files with Procrustes alignment, and click OK.



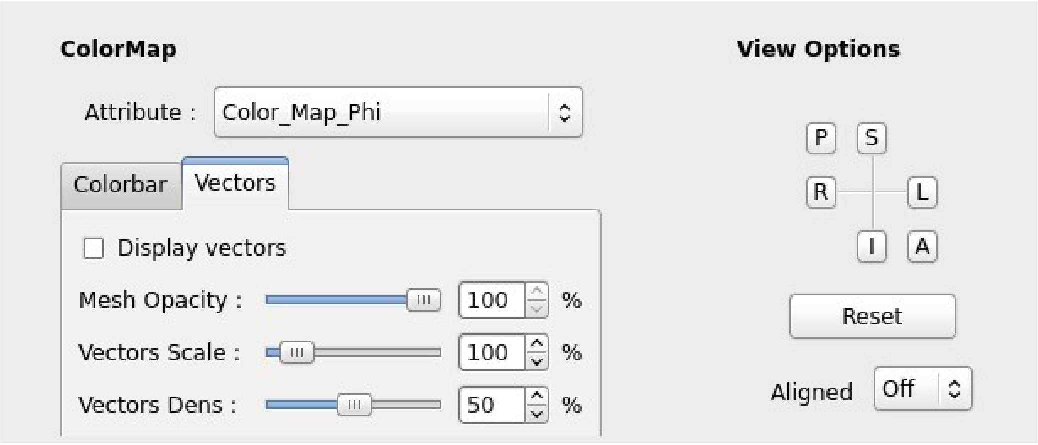
Quality control using ShapePopulationViewer

- The four output files are shown. This view show the phi correspondences between the files.
- Quality control of the correspondences is performed using the color-coded parameterization information.
- Equally colored areas represent equal correspondences.



Quality control using ShapePopulationViewer

- Locate the *Attribute* tab under *ColorMap* to toggle between phi and theta views.
- Only data sets with Procrustes alignment information are automatically aligned in *ShapePopulationViewer*.
- For data sets without Procrustes alignment:
    - Under *View Options*, set *Aligned* to *On* to align the data set using file information.



ColorMap

Attribute : Color_Map_Phi

☐ Display vectors

Mesh Opacity : 100 %

Vectors Scale : 100 %

Vectors Dens : 50 %

View Options

Aligned Off

Quality control using ShapePopulationViewer

- For more information about using *ShapePopulationViewer*, consult the *ShapePopulationViewer* tutorial by Alexis Girault:

https://www.nitrc.org/docman/view.php/759/1339/User%20Tutorial%20v1.3.2